

FIG. 1

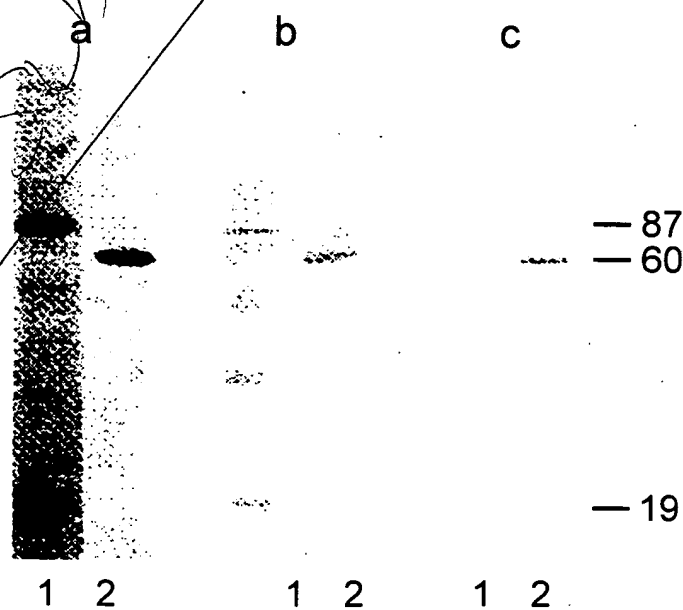


FIG. 2

09638497.082701

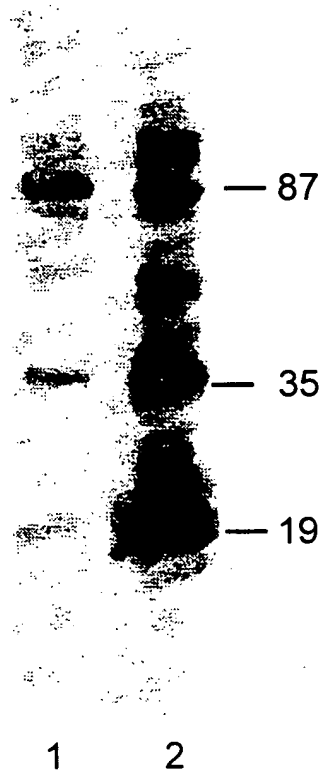


FIG. 3

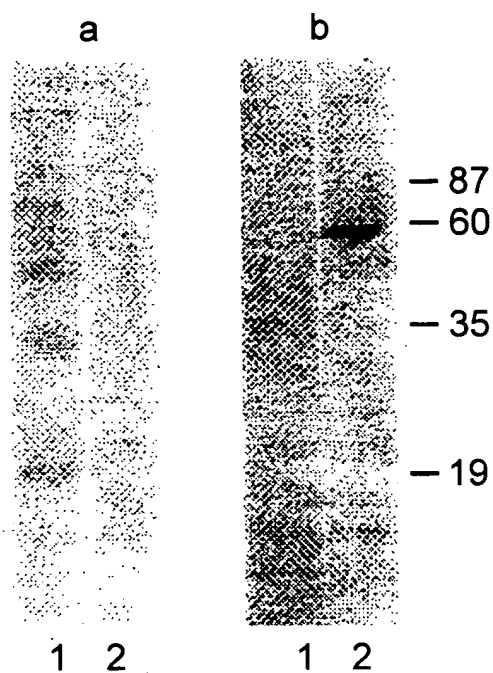


FIG. 4

0938497.082701

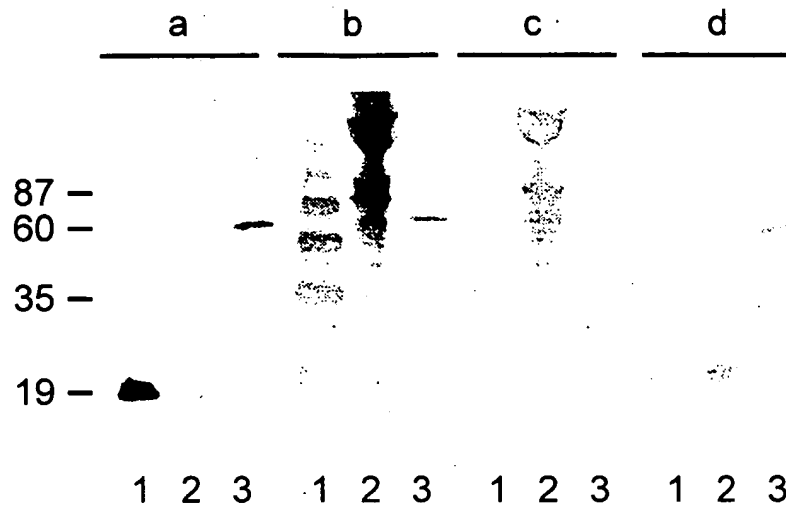


FIG. 5

0938497-086660

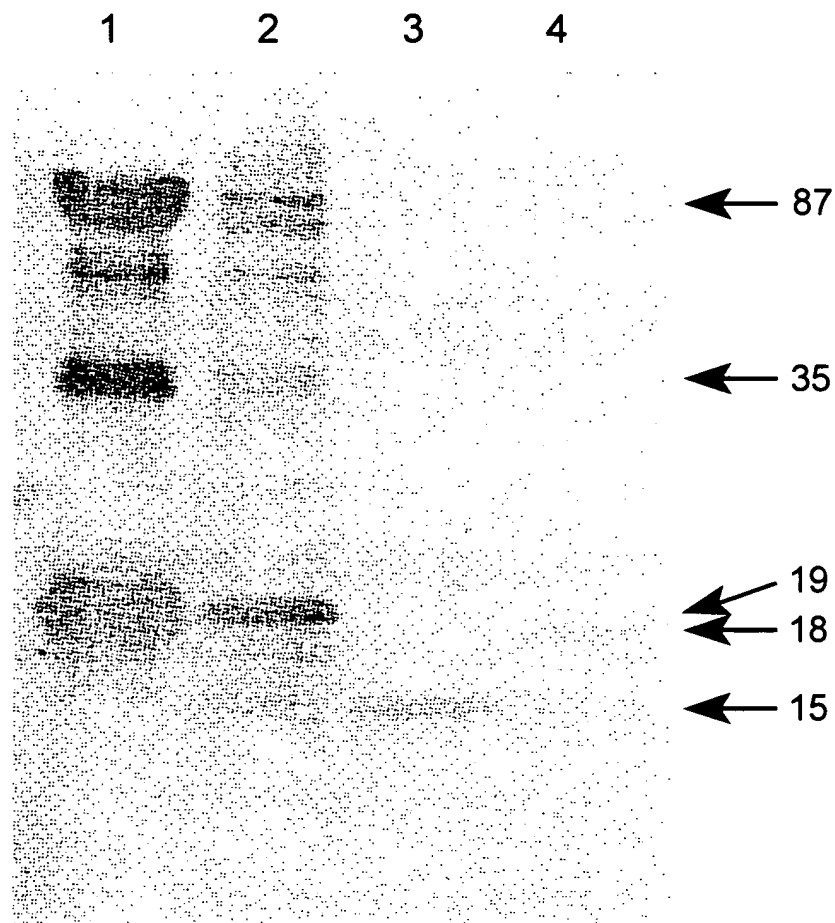


FIG. 6

05938497.082701

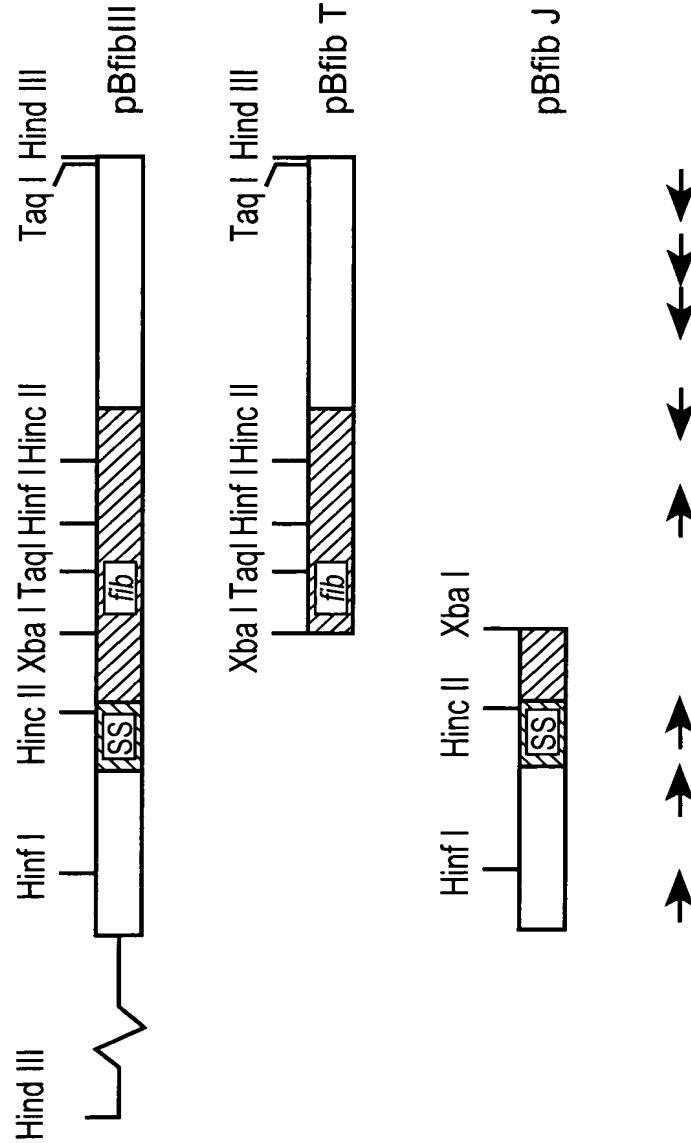


FIG. 7

1 GACTAGTGATAAGTGCTGATGAGTCACAAGATAGATAACTATATTTTGTCTATATTATA 60
 61 AAGTGTTTATAGTTAATTAATAATTAGTTAATTTCAAAAGTTGTATAAATAGGATAACTT 120
 121 AATAAATGTAAGATAATAATTGGAGGATAATTAACATGAAAAATAAATTGATAGCAAAA 180
 181 TCTTTATTAACAATAGCGGCAATTGGTATTACTACAACACTACAATTGCGTCAACAGCAGAT 240
 241 GCGAGCGAAGGATACGGTCCAAGAGAAAAGAAACCAGTGAGTATTAATCACAATATCGTA 300
 301 GAGTACAATGATGGTACTTTTAAATATCAATCTAGACCAAAATTTAACTCAACACCTAAA 360
 361 TATATTAAATTCAAACATGACTATAATATTTTAGAATTTAACGATGGTACATTGCAATAT 420
 421 GGTGCACGTCCACAATTTAATAAACCAGCAGCGAAAACCTGATGCAACTATTAATAAAAGAA 480
 481 CAAAAATTGATTCAAGCTCAAATCTTGTGAGAGAATTTGAAAAACACATACTGTCACT 540
 541 GCACACAGAAAAGCACAAAAGGCAGTCAACTTAGTTTCGTTTGAATACAAAGTGAAGAAA 600
 601 ATGGTCTTACAAGAGCGAATTGATAATGTATTAAACAAGGATTAGTGAGATAATACTTC 660
 661 TGTCATTATTTTAAGTTCAAATAATTTAATATTATATTATTTTATTAATAAAACGAC 720
 721 TATGCTATTTAATGCCAGGTTAATGTAACCTTCCTAAAATTGACTATATAATCGTTAAGT 780
 781 ATCAATTTTAAGGAGAGTTTACAATGAAATTTAAAAATATATATTAACAGGAACATTAG 840
 841 CATTACTTTTATCATCAACTGGGATAGCAACTATAGAAGGGAATAAAGCAGATGCAAGTA 900
 901 GTCTGGACAAATATTTAACTGAAAGTCAGTTTCATGATAAACGCATAGCAGAAGAATTAA 960
 961 GAACTTTACTTAACAAATCGAATGTATATGCATTAGCTGCAGGAAGCTT 1009

FIG. 8

1 ATAGATACTATATTTTGTCTATATTATAAAGTGTTTATAGTTAATTAATAATTAGTTAA 60
 1 G CA 60

61 TTTCAAAAGTTGTATAAATAGGATAACTTAATAAATGTAAGATAATAATTTGGAGGATAA 120
 61 120

121 TTAACATGAAAAATAAATTGATAGCAAAATCTTTATTAACAATAGCGGCAATTGGTATTA 180
 121 G GC T A 180

181 CTACAACTACAATTGCGTCAACAGCAGATGCGAGCGAAGGATACGGTCCAAGAGAAAAGA 240
 181 240

241 AACCAGTGAGTATTAATCACAATATCGTAGAGTACAATGATGGTACTTTTAAATATCAAT 300
 241 300

301 CTAGACCAAATTTAACTCAACACCTAAATATATTAAATTCAAACATGACTATAATATTT 360
 301 360

361 TAGAATTTAACGATGGTACATTGCAATATGGTGCACGTCCACAATTTAATAAACCAGCAG 420
 361 420

421 CGAAAACTGATGCAACTATTAAAAAAGAACAAAAATTGATTCAAGCTCAAATCTTGTGA 480
 421 480

481 GAGAATTTGAAAAACACATACTGTCAGTGCACACAGAAAAGCACAAAAGGCAGTCAACT 540
 481 540

541 TAGTTTCGTTTGAATACAAAGTGAAGAAAATGGTCTTACAAGAGCGAATTGATAATGTAT 600
 541 600

601 TAAACAAGGATTAGTGAGATAATACTTCTGTCATTATTTTAAGTTCAAAA...TAATT 660
 601 T A A AA C GC G T TC GG TAAT 660

661 TAATATTATATTATTTTTTATTAATAAAACGACTATGCTATTTAATGCCAGGTTAATGTA 720
 661 A G G A G G AA G AT A 720

721 ACTTTCCTAAAATTGACTATATAATCGTTAAGTATCAATTTTAAGGAGAGTTTACAATGA 780
 721 T G G C AG C T 780

781 AATTT 785
 781 785

FIG. 9

1 MKNKLIAKSLLTIAAIGITTTTIASTADASEGYGPREKKPVSINHNIVEYNDGTFKYQSR 60
1 A L 60
61 PKFNSTPKYIKFKHDYNILEFNDGTFEYGARPQFNKPAAKTDATIKKEQKLIQAQNLVRE 120
61 120
121 FEKTHTVSAHRKAQKAVNLVSFEYKVKKMVLQERIDNVLKQGLVR 165
121 K 165

FIG. 10

099338497.082701

FO2280" 2648E660

Fbg-bp, strain Newman:

SEGYGPR

EKKPVSINH
 KYIKFKHDY

NIVEYNDGSFK
 NILEFNDGTFE
 YQSRPKFNSTP
 YGARPOFNKPA

AKTDATIKKEQKLIQAQNLVREFEKTHTVSAHRKAQKAVNLVSFEYKVKMMVLQERIDNVLKQGLVR

Coagulase, strain 8325-4:

(C-terminal fragment)

KYVKYRDAGT	ASQ	YGPRPQFNKTP
ETNAY	GIREYNDGTFG	YEARRFNKPS
ETNAY	NVTTHANGQVS	YGARPTYKKPS
KTNAY	NVTTHANGQVS	YGARPTQNKPS
KTNAY	NVTTHANGQVS	YGARQAQNKPS
KTNAY	NVTTHANGQVS	YGARPTYKKPS
KTNAY	NVTTHADGTAT	YGPRVTK

FIG. 11

102280 2648E660

Adherence and Internalisation to fibroblasts by Newman and Newman AH12 (Eap::Ery^R) O.N culture

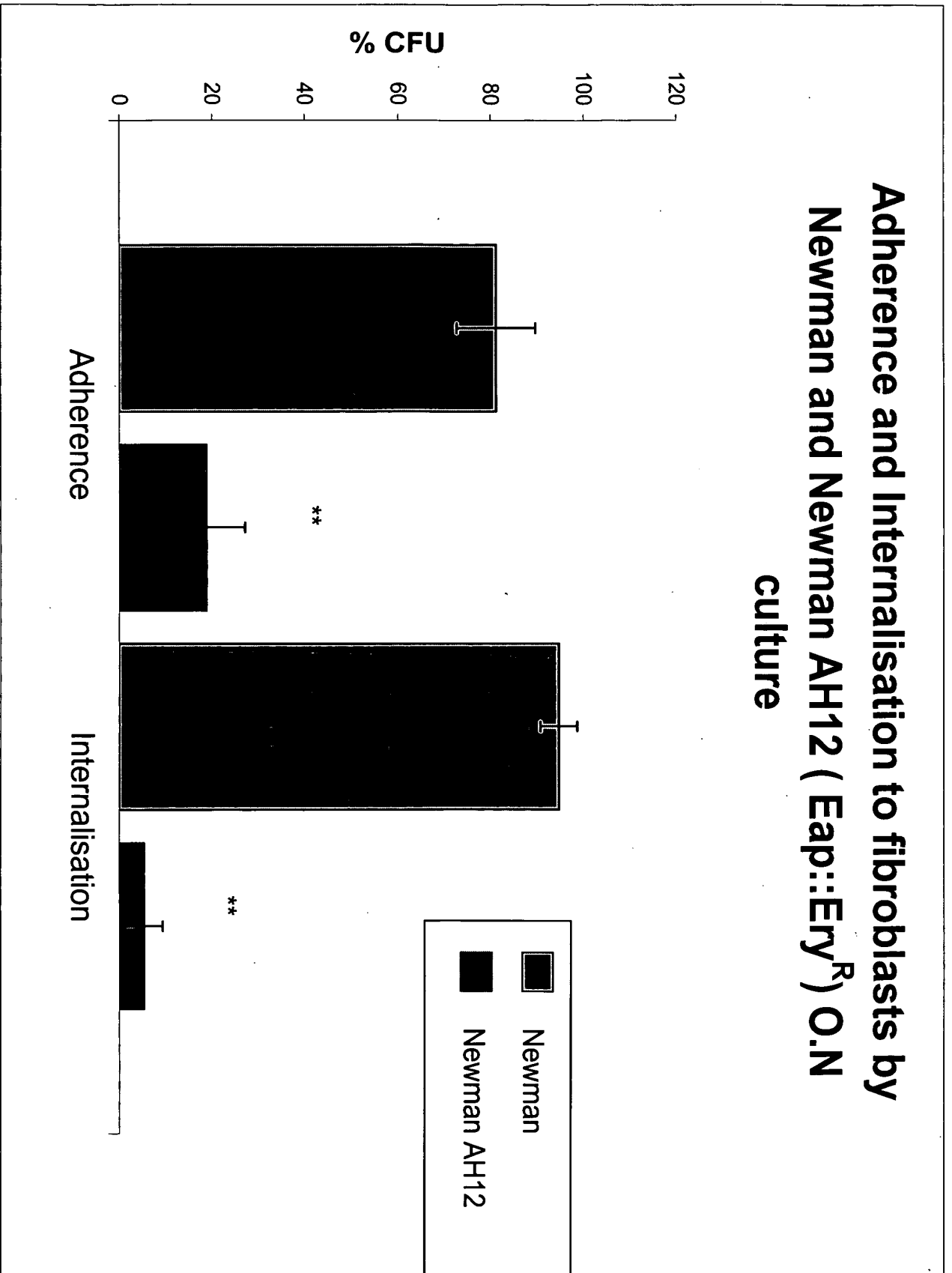


FIG. 12

102280 4548E660

Adherence and Internalization into epithelial cells of Newman and Newman AH12 (Eap::Ery^R), O.N culture

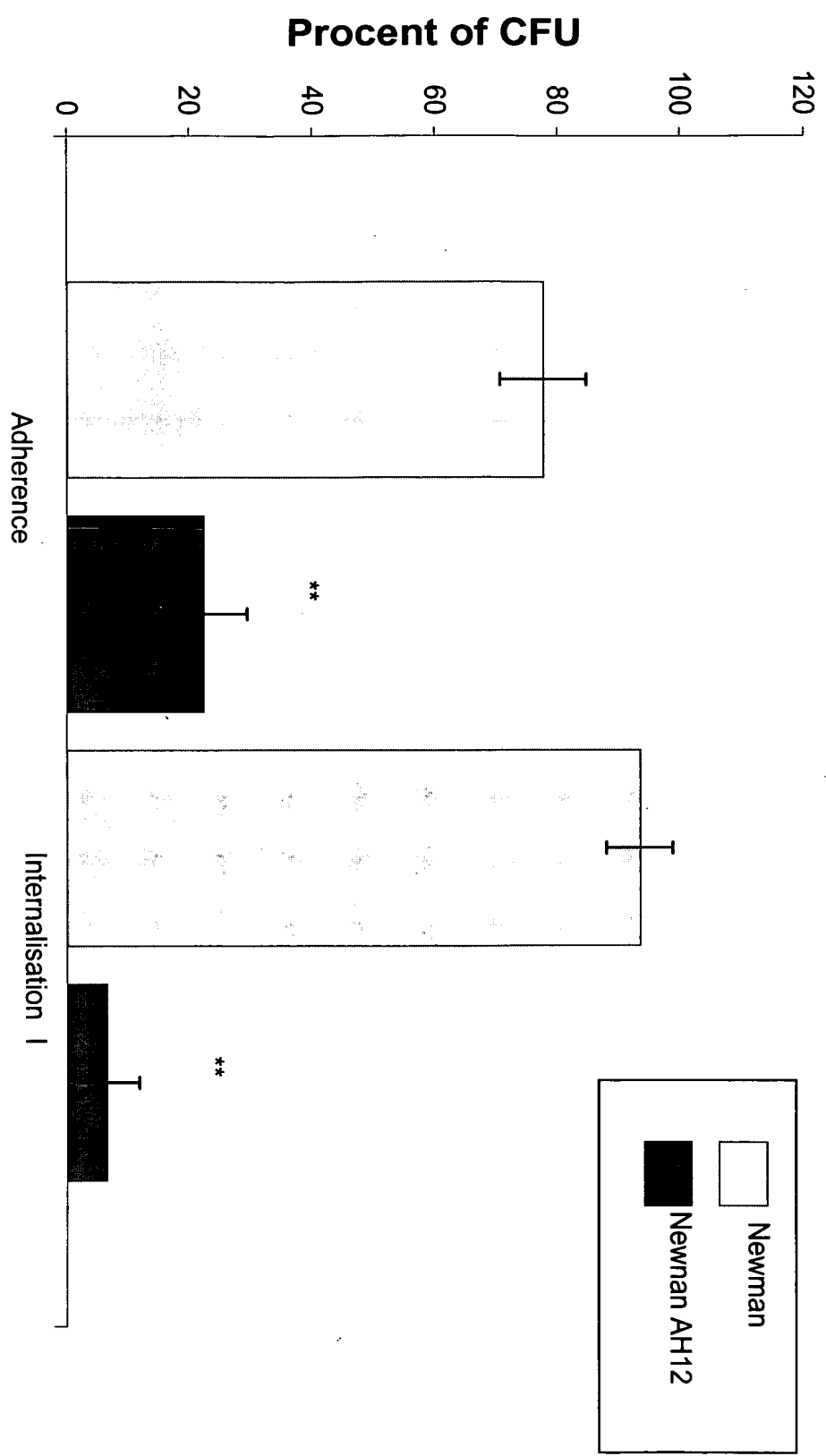


FIG. 13

102280 2648E650

Adherence and Internalisation to epithelial cells by a 2 hours culture of Newman and Newman AH12 (Eap::Ery^R)

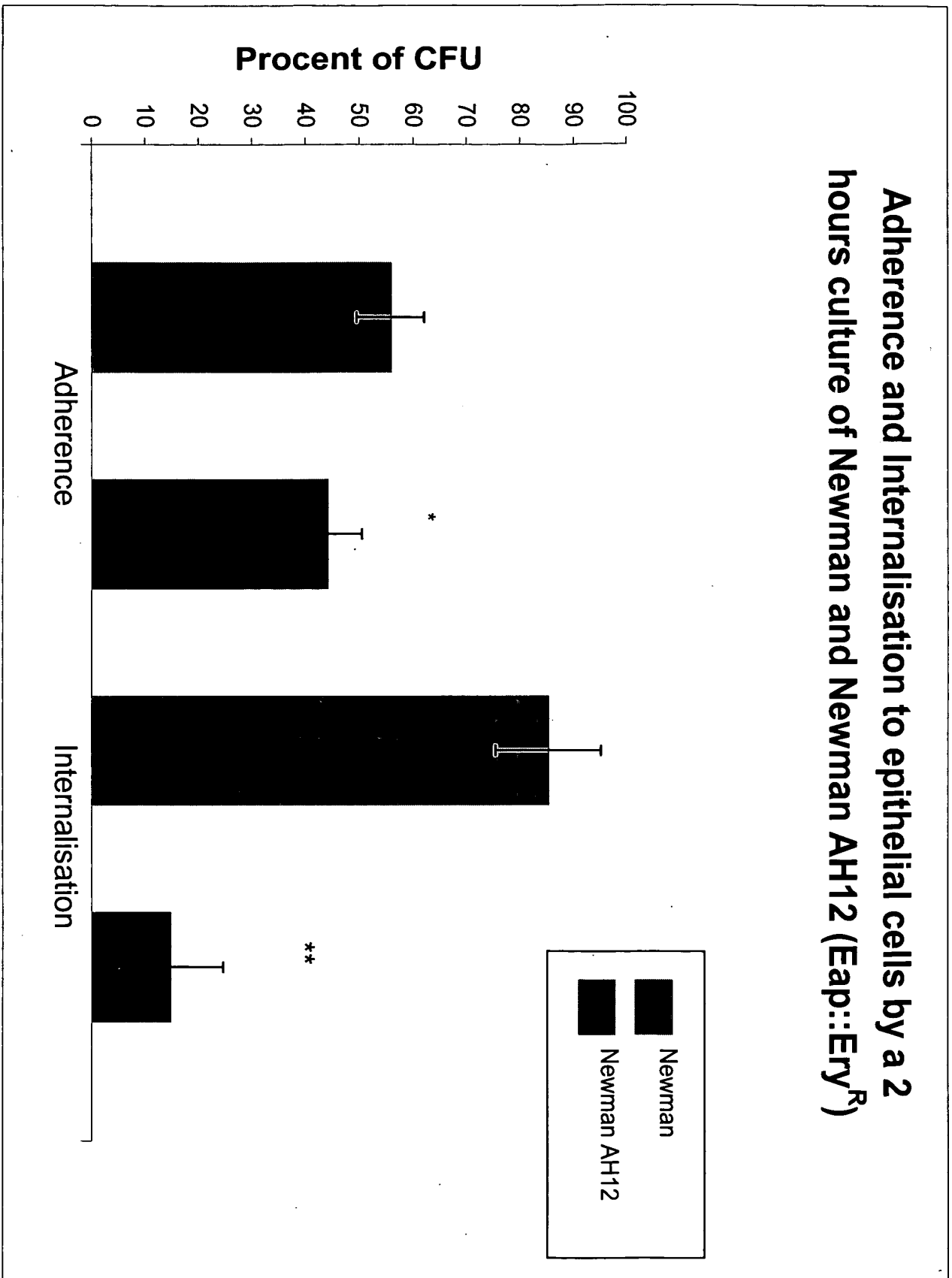


FIG. 14

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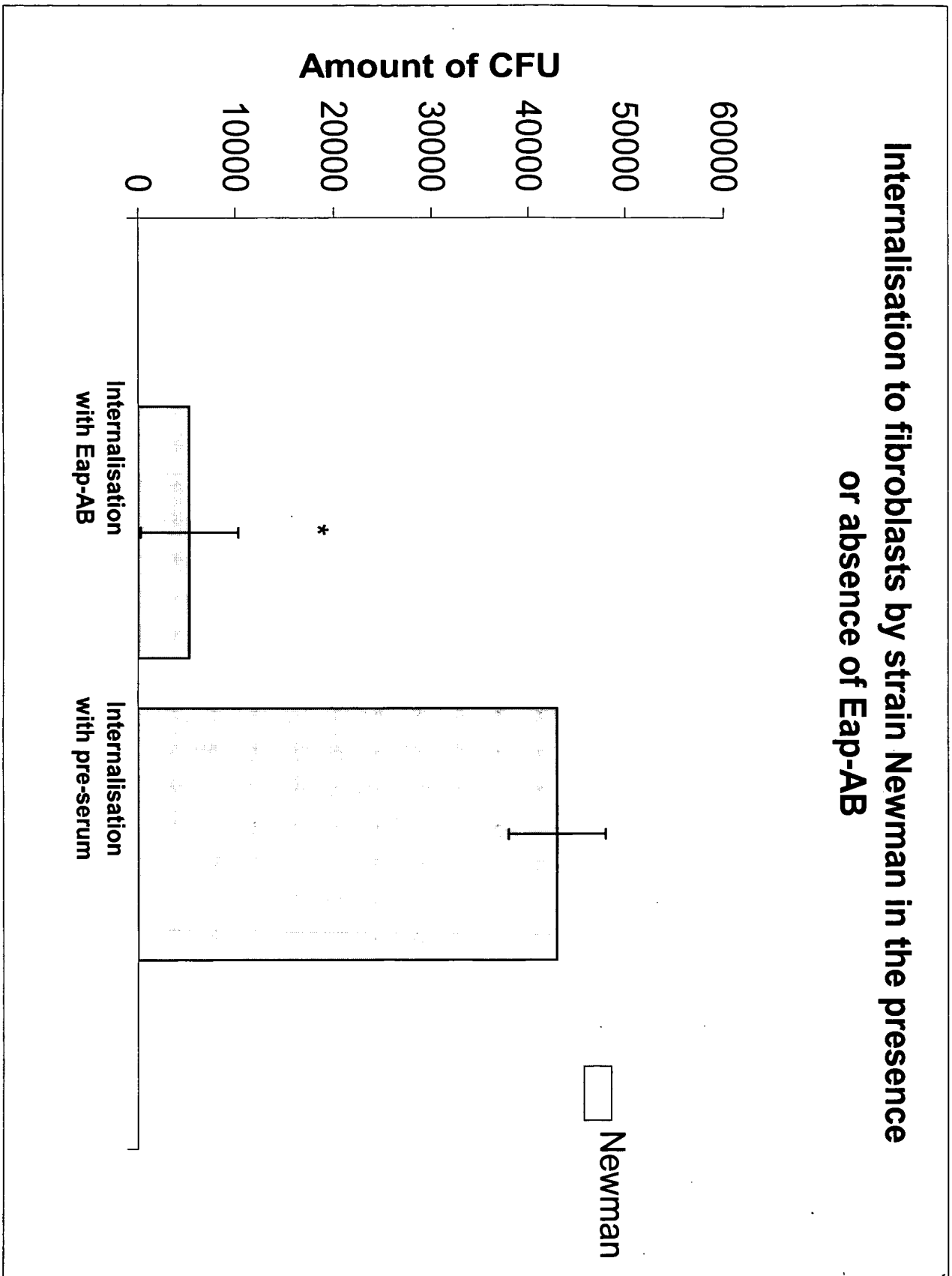


FIG. 15